

Sequence alignment showing conservation of amino acid residues across the 610-970 position range. The alignment includes 2phk_PhK and homologs from 15240873.p, 30684346.p, 15240863.p, 15240864.p, 15240865.p, AK072359.p, R0VAKVLKLCNGE, EFLNEVMS, R0VAKVLKLCNGE, 83500350.q, R0VAKVLKLCNGE, 83500348.q, R0VAKVLKLCNGE, 83520796.q, AK110482.q, AK099912.q, R0VAKVLKLCNGE, 28610021.q, R0VAKVLKLCNGE, 83500351.q, R0VAKVLKLCNGE, 29140009.q, R0VAKVLKLCNGE, AK066430.q, R0VAKVLKLCNGE, 83562326.q, STIAVKLLEDSDNNGE, 51690015.q, SEIAVAKMLLEDPTKDAE, 16904687.q, R0VAKVLKLCNGE, lir3_IRK, 1ias_TGFbR, 2phk_PhK.